

2121

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/963,790A

DATE: 02/28/2002

TIME: 11:21:53

Input Set : A:\032301.230.SEQ.ST25.txt  
 Output Set: N:\CRF3\02282002\I963790A.raw

3 <110> APPLICANT: FARWICK, Mike, et al.  
 5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE deaD GENE  
 7 <130> FILE REFERENCE: 032301 WD 230  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/963,790A  
 C--> 9 <141> CURRENT FILING DATE: 2001-09-27  
 9 <160> NUMBER OF SEQ ID NOS: 4  
 11 <170> SOFTWARE: PatentIn version 3.1  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 2381  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Corynebacterium glutamicum  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (259)..(2130)  
 21 <223> OTHER INFORMATION:  
 24 <400> SEQUENCE: 1  
 25 caggaaaccc cgcaagggtga ctcagcatca gctgacttcg ctctcgaaac cccaaaccaac 60  
 27 actgttgaag atgcaccagc atctgagggt agcgaagaga tcaccagggt tgccgatact 120  
 29 tctgaggacg ccgactctgc agatgcagac aacgcgagca atgtaatcaa tgagaatgag 180  
 31 gactcctcgg aaggtgctaa ccagccttca aacgagtcat cctctacgga agccaaatcc 240  
 33 gggttcgatg cactcgga ctg cca gag cgt gta ctt gac gct gtg cgc aag 291  
 34 Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys  
 35 1 5 10  
 37 gtg ggt tac gaa act cct tcc cca att cag gca caa acc atc cca atc 339  
 38 Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile  
 39 15 20 25  
 41 ctc atg gag ggc cag gat gtt ggt cta gca cag acc ggt acc ggt 387  
 42 Leu Met Glu Gly Gln Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly  
 43 30 35 40  
 45 aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac aag tcc 435  
 46 Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser  
 47 45 50 55  
 49 gtg cgc agc cca cag gca ctt gtg ctt gcc cct acc cgt gag cag gca 483  
 50 Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala  
 51 60 65 70 75  
 53 ctt cag gtt gac tcc ttc caa tcc ttc gct gac cac gtc ggt ggc 531  
 54 Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly  
 55 80 85 90  
 57 ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att cag ctc 579  
 58 Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu  
 59 95 100 105  
 61 tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca ggc cga 627  
 62 Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro Gly Arg

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63	110	115	120	
65	atc atc gat cac ctc gaa aag ggc tcc ctg gat atc tcc gga ctg cgc			675
66	Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg			
67	125	130	135	
69	ttc ctc gtg ctc gat gaa gca gac gag atg ctg aac atg ggc ttc cag			723
70	Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln			
71	140	145	150	155
73	gaa gat gtc gag cgc atc ctc gag gac acc cca gac gag aag cag gtt			771
74	Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val			
75	160	165	170	
77	gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg tcc aag			819
78	Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys			
79	175	180	185	
81	cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag acc agg			867
82	Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg			
83	190	195	200	
85	act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac cgc aac			915
86	Thr Asn Thr Asn Ile Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn			
87	205	210	215	
89	aag atg gat gca ctg acc cgt att ctc gag gtc acc gag ttt gaa gca			963
90	Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala			
91	220	225	230	235
93	atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt gct gaa			1011
94	Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu			
95	240	245	250	
97	aag ctc cgt gca cgc gga ttc tcc gca gca gcc atc aac ggc gac att			1059
98	Lys Leu Arg Ala Arg Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile			
99	255	260	265	
101	gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac ggc cgc			1107
102	Ala Gln Ala Gln Arg Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg			
103	270	275	280	
105	ctg gac atc ctc gtt gca acc gac gtt gca gcc cgt ggt ctt gac gtt			1155
106	Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val			
107	285	290	295	
109	gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac acc gag			1203
110	Glu Arg Ile Ser His Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu			
111	300	305	310	315
113	tcc tac gtt cac cgc atc ggc cgc acc ggc cgt gca gga cgt acc ggc			1251
114	Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly			
115	320	325	330	
117	gag gca atc ctg ttc gtg acc cca cgt gag cgt cgt atg ctt cgc tcc			1299
118	Glu Ala Ile Leu Phe Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser			
119	335	340	345	
121	atc gag cgc gca acc aac gca cca ctg cac gaa atg gaa ctg cca acc			1347
122	Ile Glu Arg Ala Thr Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr			
123	350	355	360	
125	gtc gat cag gtc aac gac ttc cgc aag gtc aag ttc gct gac tcc atc			1395
126	Val Asp Gln Val Asn Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile			
127	365	370	375	

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129 acc aag tcc ctc gag gac aag cag atg gac ctg ttc cgc acc ctg gtc	1443
130 Thr Lys Ser Leu Glu Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val	
131 380 385 390 395	
133 aag gaa tac tcc cag gcc aac gac gtt cct cta gag gac atc gca gcg	1491
134 Lys Glu Tyr Ser Gln Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala	
135 400 405 410	
137 gca ctg gca acc cag gca cag tcc ggc gac ttc ctg ctc aag gag ctc	1539
138 Ala Leu Ala Thr Gln Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu	
139 415 420 425	
141 cca cca gag cgc cgt gag cgc aac gac cgc cgt gac cgt gac ttc	1587
142 Pro Pro Glu Arg Arg Glu Arg Asn Asp Arg Arg Arg Asp Arg Asp Phe	
143 430 435 440	
145 gac gac cgt ggt gga cgt gga cgc gac cgt gac cgt ggc gac cgc gga	1635
146 Asp Asp Arg Gly Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly	
147 445 450 455	
149 gat cgt ggc tca cgc ttc gac cgc gac gac gag aac ctg gca acc tac	1683
150 Asp Arg Gly Ser Arg Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr	
151 460 465 470 475	
153 cgc ctc gca gtg ggc aag cgc cag cac atc cgc cca ggc gca atc gtt	1731
154 Arg Leu Ala Val Gly Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val	
155 480 485 490	
157 ggt gca ctt gcc aac gaa ggt ggc ctg aac tcc aag gac ttc ggc cgc	1779
158 Gly Ala Leu Ala Asn Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg	
159 495 500 505	
161 atc acc atc gca gcc gac cac acc ctg gtt gaa ctg cca aag gat ctc	1827
162 Ile Thr Ile Ala Ala Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu	
163 510 515 520	
165 cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc ggc cag	1875
166 Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln	
167 525 530 535	
169 ctc atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc cgc ttc	1923
170 Leu Ile Asn Ile Glu Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe	
171 540 545 550 555	
173 gag cgc gat gac cgt ggc gga cgc ggc gga ttc cgc ggc gac cgt gat	1971
174 Glu Arg Asp Asp Arg Gly Gly Arg Gly Phe Arg Gly Asp Arg Asp	
175 560 565 570	
177 gac cgc ggt gga cgt gga cgt gac gat cgt gga agc cgt gga	2019
178 Asp Arg Gly Gly Arg Gly Asp Arg Asp Asp Arg Gly Ser Arg Gly	
179 575 580 585	
181 ggt ttc cgc ggt gga cgt gac cgt gat gat cgt ggc gga cgc ggt gga	2067
182 Gly Phe Arg Gly Gly Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly	
183 590 595 600	
185 ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc ggt tac	2115
186 Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Gly Arg Gly Gly Tyr	
187 605 610 615	
189 cgt ggc gga cgc gac taagagttcg ttttagcttc agctcagggtt ttccgcctgag	2170
190 Arg Gly Gly Arg Asp	
191 620	
193 tctggtgctt agctagaaaa atccgttgct ctctttac tgagagggca acggattttt	2230

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195 tctgtttct taggcttgg ttcttgggg atcttgggg aggaattcta ggaacttaga 2290  
 197 gaagtaaatg atggcgcttc gaccgcagca ccatcgtaa gattctgacc aaagaagaga 2350  
 199 gcattgcgtt gctctctagt cagagtgcga g 2381  
 202 <210> SEQ ID NO: 2  
 203 <211> LENGTH: 624  
 204 <212> TYPE: PRT  
 205 <213> ORGANISM: Corynebacterium glutamicum  
 207 <400> SEQUENCE: 2  
 209 Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys Val Gly Tyr Glu Thr  
 210 1 5 10 15  
 213 Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile Leu Met Glu Gly Gln  
 214 20 25 30  
 217 Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly Lys Thr Ala Ala Phe  
 218 35 40 45  
 221 Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln  
 222 50 55 60  
 225 Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala Leu Gln Val Ala Asp  
 226 65 70 75 80  
 229 Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro  
 230 85 90 95  
 233 Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg  
 234 100 105 110  
 237 Gly Ala His Ile Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu  
 238 115 120 125  
 241 Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp  
 242 130 135 140  
 245 Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln Glu Asp Val Glu Arg  
 246 145 150 155 160  
 249 Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val Ala Leu Phe Ser Ala  
 250 165 170 175  
 253 Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn  
 254 180 185 190  
 257 Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile  
 258 195 200 205  
 261 Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu  
 262 210 215 220  
 265 Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val  
 266 225 230 235 240  
 269 Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg  
 270 245 250 255  
 273 Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg  
 274 260 265 270  
 277 Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg Leu Asp Ile Leu Val  
 278 275 280 285  
 281 Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val Glu Arg Ile Ser His  
 282 290 295 300  
 285 Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg  
 286 305 310 315 320  
 289 Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe

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290	325	330	335
293	Val Thr Pro Arg Glu Arg Arg Met	Leu Arg Ser Ile Glu Arg Ala Thr	
294	340	345	350
297	Asn Ala Pro Leu His Glu Met Glu	Leu Pro Thr Val Asp Gln Val Asn	
298	355	360	365
301	Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu		
302	370	375	380
305	Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln		
306	385	390	395
309	Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln		
310	405	410	415
313	Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg		
314	420	425	430
317	Glu Arg Asn Asp Arg Arg Asp Arg Asp Phe Asp Asp Arg Gly Gly		
318	435	440	445
321	Arg Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg		
322	450	455	460
325	Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly		
326	465	470	475
329	Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn		
330	485	490	495
333	Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala		
334	500	505	510
337	Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu Pro Gln Ser Val Leu		
338	515	520	525
341	Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln Leu Ile Asn Ile Glu		
342	530	535	540
345	Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe Glu Arg Asp Asp Arg		
346	545	550	555
349	Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg		
350	565	570	575
353	Gly Arg Asp Arg Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly		
354	580	585	590
357	Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Arg Asp		
358	595	600	605
361	Asp Arg Gly Asp Arg Gly Gly Arg Gly Gly Tyr Arg Gly Gly Arg Asp		
362	610	615	620
365	<210> SEQ ID NO: 3		
366	<211> LENGTH: 28		
367	<212> TYPE: DNA		
368	<213> ORGANISM: Corynebacterium glutamicum		
370	<400> SEQUENCE: 3		
371	gatctagaaa tccggcttcg atgcactc		28
374	<210> SEQ ID NO: 4		
375	<211> LENGTH: 28		
376	<212> TYPE: DNA		
377	<213> ORGANISM: Corynebacterium glutamicum		
379	<400> SEQUENCE: 4		
380	ctaagcttcg acgggtggca gttccatt		28

**VERIFICATION SUMMARY**

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Input Set : A:\032301.230.SEQ.ST25.txt

Output Set: N:\CRF3\02282002\I963790A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date